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BLink, Conserved
Domains, Links

■ 1: AAG12684. Reports myb-related prote...[gi:10092271]

Comment Features Sequence

LOCUS AAG12684 126 aa linear PLN 22-JAN-2001
 DEFINITION myb-related protein; 20671-21051 [Arabidopsis thaliana].
 ACCESSION AAG12684
 VERSION AAG12684.1 GI:10092271
 DBSOURCE locus AC025814 accession AC025814.7
 KEYWORDS .
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (residues 1 to 126)
 REFERENCE AUTHORS Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
 Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
 Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
 TITLE Arabidopsis thaliana chromosome 1 BAC F22H5 genomic sequence
 JOURNAL Unpublished
 REFERENCE AUTHORS Lin,X. and Kaul,S.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
 REFERENCE AUTHORS Town,C.D. and Kaul,S.
 TITLE Direct Submission
 JOURNAL Submitted (12-SEP-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
 REFERENCE AUTHORS Town,C.D. and Kaul,S.
 TITLE Direct Submission
 JOURNAL Submitted (05-OCT-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
 REFERENCE AUTHORS Town,C.D. and Kaul,S.
 TITLE Direct Submission
 JOURNAL Submitted (12-OCT-2000) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
 REFERENCE AUTHORS Town,C.D. PhD.
 TITLE Direct Submission
 JOURNAL Submitted (22-JAN-2001)
 COMMENT Address all correspondence to:at@tigr.org

 BAC clone F22H5 is from Arabidopsis thaliana chromosome 1
 The orientation of the sequence is from SP6 to T7 end of the BAC
 clone.
 Genes were identified by a combination of several methods: Gene
 prediction programs including Genscan+ (Chris Burge,

<http://CCR-081.mit.edu/GENSCAN.html>), GeneMarkHMM (Mark Borodovsky, <http://genemark.biology.gatech.edu/GeneMark/>), GlimmerA (a variant of GlimmerM, see Mihaela Pertea, <http://www.tigr.org/softlab/glimmerm.htm/glimmerm.html>, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/tgi.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Method: conceptual translation.

FEATURES

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Location/Qualifiers
1..126
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[/db_xref="taxon:3702"](#)
[/chromosome="1"](#)
[/clone="F22H5"](#)
[/ecotype="Columbia"](#)

Protein

1..126
[/product="myb-related protein; 20671-21051"](#)

Region

11..54
[/region_name="SANT"](#)
[/note="SANT SWI3, ADA2, N-CoR and TFIIIB' DNA-binding domains; smart00717"](#)
[/db_xref="CDD:47985"](#)

CDS

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[/gene="F22H5.3"](#)
[/coded_by="AC025814.7:20955..21335"](#)

ORIGIN

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61 linietgrvp lpnyktfesn srsindfdtr yitkylymml siyfdnhssd fekfsqkv lv
121 syislv

//

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